

Amendments to the Claims:

This listing of claims will replace all prior versions and listings of claims in the application.

Listing of Claims:

Claims 1-20 (canceled)

Claim 21 (currently amended): A transgenic plant transformed with an expression vector comprising a polynucleotide sequence encoding a polypeptide having a conserved domain that has at least 70% sequence identity to the conserved domain of amino acid coordinates 111-164 of SEQ ID NO: 194, wherein the conserved domain is required for a function by the polypeptide of regulating transcription and the polypeptide confers to the transgenic plant greater tolerance to water deprivation than a control plant.

Claim 22 (previously presented): The transgenic plant of claim 21, wherein the expression vector further comprises a constitutive, inducible, or tissue-specific promoter operably linked to the polynucleotide sequence.

Claim 23 (previously presented): A seed produced by the transgenic plant according to claim 21, wherein the seed comprises the polynucleotide sequence of claim 21.

Claim 24 (currently amended): A method for producing a transgenic plant having ~~an altered trait as compared to a wild type plant of the same species~~ greater tolerance to water deprivation than a control plant, the method steps comprising:

- (a) providing an expression vector comprising:
 - (i) a polynucleotide sequence encoding a polypeptide comprising a conserved domain that has at least 70% sequence identity to the conserved domain of amino acid coordinates 111-164 of SEQ ID NO: 194, wherein the conserved domain is required for a function by the polypeptide of regulating transcription and the polypeptide confers to the transgenic plant greater tolerance to water deprivation than the control plant; and
 - (ii) at least one regulatory element operably linked to the polynucleotide sequence, wherein said at least one regulatory element controls expression of the polynucleotide sequence in a target plant;
- (b) introducing the expression vector into at least one plant; and
- (c) selecting at least one transgenic plant that has ~~an altered trait as compared to a wild type plant of the same species~~ greater tolerance to water deprivation than the control plant;

~~wherein the altered trait is selected from the group consisting of greater tolerance to cold during germination, greater tolerance to cold during growth, greater tolerance to water deprivation, greater tolerance to nitrogen limitation, larger leaves, and greater biomass than the wild-type plant.~~

Claim 25 (currently amended): The method of claim 24, wherein the polypeptide comprises a conserved domain that has at least ~~75%~~ 80% sequence identity to the conserved domain of amino acid coordinates 111-164 of SEQ ID NO: 194.

Claim 26 (currently amended): The method of claim 24, wherein the polypeptide comprises a conserved domain that has at least ~~80%~~ 85% sequence identity to the conserved domain of amino acid coordinates 111-164 of SEQ ID NO: 194.

Claim 27 (previously presented): The method of claim 24, wherein the regulatory element is a cauliflower mosaic virus 35S promoter.

Claim 28 (currently amended): The method of claim 24, wherein the regulatory element is a root-specific, epidermis-specific, meristem-specific, vascular-specific or leaf-specific promoter.

Claim 29 (previously presented): The method of claim 24, wherein the regulatory element is a drought-inducible or cold-inducible promoter.

Claim 30 (canceled)

Claim 31 (currently amended): The method of claim 24, wherein the transgenic plant has greater tolerance to 168 hours without watering than the ~~wild-type~~ control plant.

Claims 32-33 (canceled)

Claim 34 (previously presented): A seed produced by a transgenic plant produced by the method according to claim 24, wherein the seed comprises the expression vector of claim 24.

Claim 35 (currently amended): A method for increasing the tolerance of a plant to ~~an abiotic stress~~ water deprivation, the method steps comprising:

(a) providing an expression vector comprising:

- (i) a polynucleotide sequence encoding a polypeptide comprising a conserved domain that has at least 70% sequence identity to the conserved domain of amino acid coordinates 111-164 of SEQ ID NO: 194, wherein the conserved domain is required for a function by the polypeptide of regulating transcription and the polypeptide confers to the transgenic plant greater tolerance to water deprivation than a control plant; and
- (ii) at least one regulatory element flanking the polynucleotide sequence, wherein said at least one regulatory element controls expression of the polynucleotide sequence in a target plant;
- (b) introducing the expression vector into a plant, thereby producing a transgenic plant; and
- (c) selecting a transgenic plant having ~~an altered trait as compared to a wild-type plant of the same species~~ greater tolerance to water deprivation than a control plant;
~~wherein the abiotic stress is selected from the group consisting of cold stress during germination, cold stress during growth, water deprivation, and nitrogen limitation.~~

Claim 36 (currently amended): The method of claim 35, wherein the polypeptide comprises a conserved domain that has at least ~~75%~~ 80% sequence identity to the conserved domain of amino acid coordinates 111-164 of SEQ ID NO: 194.

Claim 37 (currently amended): The method of claim 35, wherein the polypeptide comprises a conserved domain that has at least ~~80%~~ 85% sequence identity to the conserved domain of amino acid coordinates 111-164 of SEQ ID NO: 194.

Claim 38 (currently amended): The method of claim 35, wherein the transgenic plant has greater tolerance to 168 hours without watering than the ~~wild-type~~ control plant.

Claims 39-40 (canceled)

Claim 41 (new) The transgenic plant of claim 21, where in the polynucleotide sequence comprises SEQ ID NO: 193.

Claim 42 (new) The method of claim 24, where in the polynucleotide sequence comprises SEQ ID NO: 193.

Claim 43 (new) The method of claim 35, where in the polynucleotide sequence comprises SEQ ID NO: 193.